





Db 361 ccagtgactatttccacagggactaagaagaactatgatgtgagaagagtaac 420  
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QY 1355 CCACTGACTAATTTTGCACAGGGTACTAAAGAACTATGATGTGAGAAAGAGACTAAC 1414  
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Db 421 atctccccaataaaccccaaatgttaatccaactctcagat 463  
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QY 1415 ATCTCTCCATTAACCCCAATAGTTATCACTCTCAGAT 1457  
|||||  
RESULT 3 AA195113 530 bp mRNA EST 17-JAN-1997  
LOCUS  
DEFINITION zr35a03.r1 Soares Nhmpu S1 Homo sapiens CDNA clone 665356 5'.  
ACCESSION AA195113  
NID 91784803  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 530)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
TITLE  
JOURNAL  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
High quality sequence stop: 257.  
Location/Qualifiers  
FEATURES  
source  
1..530  
/organism="Homo sapiens"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NBHM, pregnant uterus  
NBHPU, and fetal heart NBH19M) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."  
/clone\_1lb="665356"  
/clone\_1lb="Soares Nhmpu S1"  
/lab\_host="DH10B"  
BASE COUNT 170 a 96 c 93 g 168 t 3 others  
ORIGIN  
Query Match 21.9%; Score 335; DB 16; Length 530;  
Best Local Similarity 97.7%; Pred. No. 0.00e+00;  
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Db 1 acaaatgtatcacaagaattatttttagaagaatagatgaacacagtcacagtaaaa 60  
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QY 1178 ACAATATGTATCAGAGTATTATTAGAAATGATGATACCAAGTCCAAATCAATAAA 1237  
|||||  
Db 61 taagctcttaactgaatgacatgacatgctgttccccaatggagatccca 120  
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QY 1238 TAACTGCTTAACTGGAATGGCCATTGAGCTGTTCCCAATTTGGCGAATCCCA 1237  
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Db 121 tgaatgaataacgtttctcaggcaacttgaggtcttcagtgatcatcttctcattacca 180  
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QY 1298 TGCATGATTAAGTCTTTCTCAGGCACTTGAGGCTTCACTGATATCTTTCATTACCA 1357  
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Db 181 gtgactaatttccacagggactaagaagaactatgatgtgagaagagtaacatc 240  
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QY 1358 GTACTAATTTTCCACAGGGTACTAAAGAACTATGATGTGAGAAAGAGACTAACATC 1417  
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Db 241 tctccaataaaccccaaatgttaatccaactgtcagatctgtgactgtatctatcagac 300  
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QY 1418 TCCTCAATTAACCCCAATAGTTATCCACATCTGATCTGATCTGATCTGATCTGATC 1477  
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Db 301 tatacttcccttactactgctgctgtaattcgcactggaataaaaaa 350  
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QY 1478 TATATTTTCCCTTATTAAGTCTGCTGAGTATCACTGAGAAAAA 1527  
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RESULT 4 AA195113 530 bp mRNA EST 14-FEB-1997  
LOCUS  
DEFINITION zr35a03.r1 Soares Nhmpu S1 Homo sapiens CDNA clone 665356 5'.  
ACCESSION AA195113  
NID 91784803  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 530)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
TITLE  
JOURNAL  
COMMENT  
Contact: Wilson RK  
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Washington University School of Medicine  
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Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
High quality sequence stop: 257.  
Location/Qualifiers  
FEATURES  
source  
1..530  
/organism="Homo sapiens"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NBHM, pregnant uterus  
NBHPU, and fetal heart NBH19M) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
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reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."  
/clone\_1lb="665356"  
/clone\_1lb="Soares Nhmpu S1"  
/issue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
BASE COUNT 170 a 96 c 93 g 168 t 3 others  
ORIGIN  
Query Match 21.9%; Score 335; DB 54; Length 530;  
Best Local Similarity 97.7%; Pred. No. 0.00e+00;  
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Db 1 acaaatgtatcacaagaattatttttagaagaatagatgaacacagtcacagtaaaa 60  
|||||

Seq	Sequence	105 BP	57 A	13 C	21 G	14 T	0 other
Db	48	aaagcaaatggtgaaaaaagcaaaaaaacacacaa	86				
Qy	957	AAAGAAAGTGGAGCGAGACATTGAAAAAACAATAAA	995				
RESULT	6	standard: RNA; EST: 107 BP.					
ID	MAA17046	standard: RNA; EST: 107 BP.					
AC	AA117046:						
NI	91672122						
DT	17-NOV-1996 (Rel. 49, Created)						
DT	18-FEB-1997 (Rel. 51, Last updated, Version 2)						
DE	ms3f02.r1 Soares 2NbMt Mus musculus cDNA clone 572955 5'.						
KW	EST.						
OS	Mus musculus (house mouse)						
OC	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;						
OC	Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;						
CC	Mus.						
RP	11						
RP	1-107						
RA	Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,						
RA	Dubugue T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,						
RA	Morris M., Schellenberg K., Stepien M., Tan F., Underwood K.,						
RA	Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,						
RA	Waterston R.,						
RT	"The WashU-HMT Mouse EST Project";						
RL	Unpublished.						
CC	Contact: Marra M/Mouse EST Project WashU-HMT Mouse EST Project						
CC	Washington University School of Medicine 444 Forest Park Parkway,						
CC	Box 8001, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810						
CC	Email: mouseest@wustl.edu This image is available						
CC	royalty-free through LNL; contact the IMAGE Consortium						
CC	(info@image.lln.gov) for further information. MGI:347603 Putative						
CC	full length read vector to vector length is 108 Seq primer: -28M13						
CC	rev2 from Amersham.						
EH	Key						
FT	Location/Qualifiers						
FT	source						
FT	1..107						
FT	/organism="Mus musculus"						
FT	/strain="C57BL/6J"						
FT	/note=Vector: pUT3D-Pac (Pharmacia) with a modified						
FT	polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA						
FT	was primed with a Not I - oligo(dT) primer [5'						
FT	TGTTACCAATCTGAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT						
FT	3']; double-stranded cDNA was ligated to Eco RI adaptors						
FT	(Pharmacia), digested with Not I and cloned into the Not I						
FT	and Eco RI sites of the modified pUT3D vector. RNA provide						
FT	d						
FT	by Dr. Bertrand Jordan. Library went through two rounds of						
FT	normalization, and was constructed by Bento Soares and						
FT	M.Patima BonaIdo."						
FT	/clone="572955"						
FT	/sex="male"						
FT	/tissue_type="Thymus"						
FT	/dev_stage="4 weeks"						
FT	/lab_host="DH10B"						
FT	<1..>107						
FT	Sequence 107 BP; 50 A; 16 C; 24 G; 17 T; 0 other;						
Query Match	1.4%; Score 21; DB 91; Length 105;						
Best Local Similarity	76.9%; Pred. No. 9.46e-03;						
Matches	30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;						
Db	65	aaagcaaatggtgaaaaaagcaaaaaaacacacaa	103				
Qy	957	AAAGAAAGTGGAGCGAGACATTGAAAAAACAATAAA	995				

ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
AUTHORS	1 (bases 1 to 156)			
TITLE	European Drosophila Mapping Consortium.			
JOURNAL	Direct Submission			
COMMENT	Submitted (15-APR-1996) Michael Ashburner, Department of Genetics Downing St., Cambridge CB2 3EH, England			
STX_name	DM36D7S			
clone_name	36D7			
STX_from_promoter	= SP6			
vector_class	= cosmid, Lorist 6			
origin_of_clone	= Oregon-R			
in_situ_site_primary	= 98C			
BLAST_program	= BLASTN			
database_searched	= EMBL			
database_version	= 45.0 and updates till date_of_search			
date_of_search	= 08-01-1996			
BLAST_program	= BLASTX			
database_searched	= SWISSPROT			
database_version	= 32.0			
date_of_search	= 15-12-1995.			
location/Qualifiers				
1..156				
/organism	= "Drosophila melanogaster"			
/strain	= "Oregon-R"			
/clone	= "36D7"			
BASE COUNT	28 a	37 c	30 g	27 t
ORIGIN	34 others			
Query Match	1.4%	Score 21;	DB 36;	Length 156;
Best Local Similarity	16.2%;	Pied. No. 9.46e-03;		
Matches	6;	Conservative	23;	Mismatches 8; Indels 0; Gaps 0;
Db	24	ssrrgrcgrkrrgagsgksksrrgkckrksrgsg	60	
Cp	37	CCGGAACCTCAGGGGCTTGAGGCGGCGGCGGCG 1		
RESULT	9			
LOCUS	HUMU5145	194 bp	DNA	STS
DEFINITION	Human STS UT5145.			
ACCESSION	L17708			
NID	9308208			
KEYWORDS	PCR primer; STS sequence; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site.			
SOURCE	Homo sapiens DNA.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 194)			
AUTHORS	Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,K., Bradley,P., Eisner,T., Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome			
TITLE	Unpublished (1993)			
JOURNAL	Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics			
COMMENT	2160 Eccles Institute of Human Genetics			
	Salt Lake City, UT 84112			
	e-mail: sts@corona.med.utah.edu			
	Primer A: CTACACGAGGAGCAGAC			
	Primer B: ACCAATCCACTTCACCTTACA			
	32P-label: A Primer			
	PCR Profile:			
	Initial Denaturation: 94C 30sec			
	PCR Cycles: 5			
	Denaturation: 94C 10sec			
	Annealing: 58C 10sec			
	Extension: 72C 20sec			
	Mg++ 1mM			



Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: TGTTCGTAGTTCGTTGTTATTTGCA  
Primer B: AAAGAGTCAAAATGGGTTTTT  
STS size: 100

PCR Profile:

Presoak:

Denaturation:  
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

Location/Qualifiers

source 1..245

STS /organism="Homo sapiens"

/map="791\_B\_4; 816\_F\_6; 921\_C\_9; 928\_A\_7; 934\_F\_6;

963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

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963\_G\_6"

/map="791\_B\_4; 816\_F\_6; 921\_C\_9; 928\_A\_7; 934\_F\_6;

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: CATTCGTTTCATACATACATTC

Primer B: CACAGTGTGAGCGCTGC

STS size: 225

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from Z38433 -- dbEST.

Location/Qualifiers

source 1..253

STS /organism="Homo sapiens"

/map="923\_H\_8; 959\_F\_5; 441.7 CR from top of Chr17 linkage

group"

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group"

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

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Email: thudson@genome.wi.mit.edu

Primer A: CATTCGTTTCATACATACATTC

Primer B: CACAGTGTGAGCGCTGC

STS size: 225

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

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source 1..253

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group"

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group"

